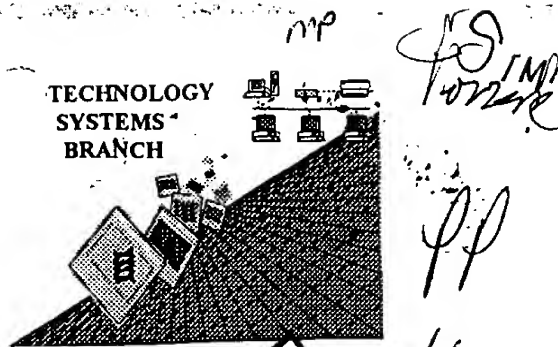


## RAW SEQUENCE LISTING ERROR REPORT

TECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/890,752  
Source: PCT09  
Date Processed by STIC: 08/14/2001

RECEIVED  
STIC CENTER 1000/2000  
DEC 8 2003

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/890,752

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos: The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4      Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7      Skipped Sequences  
    (OLD RULES) Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
  
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES) Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000
  
- 9 ✓      Use of n's or Xaa's  
    (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220> Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 06/04/2001

**The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.**

PCT09

## RAW SEQUENCE LISTING

DATE: 08/14/2001

PATENT APPLICATION: US/09/890,752

TIME: 11:17:14

Input Set : A:\PTO.txt

Output Set: N:\CRF3\08142001\I890752.raw

6 <110> APPLICANT: Eberhard Hildt, Prof. Hofschneider  
 8 <120> TITLE OF INVENTION: Particles for Gene Therapy  
 10 <130> FILE REFERENCE: 319-2 US  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/890,752  
 C--> 13 <141> CURRENT FILING DATE: 2001-08-03  
 15 <150> PRIOR APPLICATION NUMBER: DE 199 04 800.2  
 16 <151> PRIOR FILING DATE: 1999-02-05  
 18 <160> NUMBER OF SEQ ID NOS: 19  
 20 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 347  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Artificial sequence ✓  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Description of the artificial sequence: ✓  
 30 Fusion protein comprising a LHBs and heterologous binding site  
 31 RGD  
 34 <400> SEQUENCE: 1  
 36 Met Gly Arg Gly Asp Gly Ala Gly Ala Phe Gly Leu Gly Phe Thr Pro  
 37 1 5 10 15  
 39 Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu  
 40 20 25 30  
 42 Glu Thr Leu Pro Ala Asn Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser  
 43 35 40 45  
 45 Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu Arg Asn Thr His Pro  
 46 50 55 60  
 48 Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Thr Leu Gln Asp  
 49 65 70 75 80  
 51 Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly  
 52 85 90 95  
 54 Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe  
 55 100 105 110  
 57 Ser Arg Ile Gly Asp Pro Ala Leu Asn Met Glu Asn Ile Thr Ser Gly  
 58 115 120 125  
 60 Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr  
 61 130 135 140  
 63 Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu  
 64 145 150 155 160  
 66 Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser  
 67 165 170 175  
 69 Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Thr Cys Pro Gly  
 70 180 185 190  
 72 Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu  
 73 195 200 205  
 75 Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met  
 76 210 215 220  
 78 Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr Gly

Does Not Comply  
 Corrected Diskette Needed  
 See page 6 of 7A

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/890,752

DATE: 08/14/2001

TIME: 11:17:14

Input Set : A:\PTO.txt

Output Set: N:\CRF3\08142001\I890752.raw

```

79      225      230      235      240
81      Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Tyr Pro
82              245      250      255
84      Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro
85              260      265      270
87      Ile Pro Ser Ser Trp Ala Phe Gly Lys Phe Leu Trp Glu Trp Ala Ser
88              275      280      285
90      Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe
91              290      295      300
93      Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp
94      305      310      315      320
96      Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Leu Ser Pro Phe Leu Pro Leu
97              325      330      335
99      Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
100              340      345
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 215
106 <212> TYPE: PRT
107 <213> ORGANISM: Artificial sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Description of the artificial sequence:
111      Fusion protein comprising a HBcAg, a cell-permeability-
112      mediating polypeptide and heterologous binding site RGD
115 <400> SEQUENCE: 2
117      Met Pro Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Thr Val Gln
118      1      5      10      15
120      Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile Asp Pro
121              20      25      30
123      Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser
124              35      40      45
126      Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu
127              50      55      60
129      Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr
130      65      70      75      80
132      Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala
133              85      90      95
136      Thr Trp Val Gly Val Asn Leu Glu Asp Pro Glu Phe Arg Gly Asp Ala
137              100      105      110
139      Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
140              115      120      125
142      Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
143              130      135      140
145      Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
146      145      150      155      160
148      Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
149              165      170      175
151      Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Thr
152              180      185      190
154      Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser

```

## RAW SEQUENCE LISTING

DATE: 08/14/2001

PATENT APPLICATION: US/09/890,752

TIME: 11:17:14

Input Set : A:\PTO.txt

Output Set: N:\CRF3\08142001\I890752.raw

```

155          195          200          205
157      Gln Ser Arg Glu Pro Gln Cys
158          210          215
163 <210> SEQ ID NO: 3
164 <211> LENGTH: 663
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of the artificial sequence:
170      DNA coding for a fusion protein comprising a HBcAg, a cell-
171      permeability-mediating polypeptide and heterologous binding
172      site RGD
175 <400> SEQUENCE: 3
178 atgcccataat cgtcaatctt ctcgaggatt ggggaccctg gatccactac tgttcaagcc      60
180 tccaagctgt gccttgggtg gctttggggc atggacatcg acccttataa agaatttgga      120
182 gctactgttg agttactctc gtttttgccct tctgacttct ttccttcagt acgagatctt      180
184 ctagataaccg cctcagctct gtatcgggaa gccttagagt ctctgagca ttgttcacct      240
186 caccatactg cactcaggca agcaattctt tgctgggggg aactaatgac tctagctacc      300
188 tgggtgggtg ttaatttgga agatccagaa ttccgaggcg acgcgtctag agacctagta      360
190 gtcagttatg tcaacactaa tatgggccta aagttcaggc aactcttggt gtttcacatt      420
192 tcttgtctca cttttggaag agaaaccgtt atagagtatt tgggtgtctt cggagtgttg      480
194 attcgcactc ctccagctta tagaccacca aatgccccta tcctatcaac acttccggaa      540
196 actactgttg ttagacgacg aggcaggtcc cctagaagaa gaactccctc gcctgcaga      600
198 cgaaggtctc aatcgccgcg tcgcagaaga tctcaatctc gggaacctca atgttagtat      660
200 tcc
204 <210> SEQ ID NO: 4
205 <211> LENGTH: 1047
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of the artificial sequence:
211      DNA coding for a fusion protein comprising a LHBS and
212      heterologous binding site RGD
216 <400> SEQUENCE: 4
219 atgggccgtg gcgaaggagc tggagcattc gggctgggtt tcaccccacc gcacggaggc      60
221 cttttggggt ggagccctca ggctcagggc atactacaaa ctttgccagc aaatccgcct      120
223 cctgcctcca ccaatcgcca gacaggaagg cagcctaccc cgctgtctcc acctttgaga      180
225 aacactcatc ctcaggccat gcagtggaat tccacaacct ttcaccaaac tctgcaagat      240
227 cccagagtga gaggcctgta tttccctgct ggtggctcca gttcaggagc agtaaaccct      300
229 gttccgacta ctgcctctcc cttatcgtoa atcttctcga ggattgggga cctgcgctg      360
231 aacatggaga acatcacatc aggattccta ggacccttc tcgtgttaca ggcggggttt      420
233 ttcttgttga caagaatcct cacaataaccg cagagtctag actcgtgggt gacttctctc      480
235 aattttctag ggggaactac cgtgtgtctt ggccaaaatt cgcagtcccc aacctccaat      540
237 cactcaccaa cctcctgtcc tccaacttgt cctggttacc gctggatgtg tctgcggcgt      600
239 tttatcatct tcctcttcat cctgctgcta tgccctcatc tcttgttggt tcttctggac      660
241 tatcaaggta tgttgccgtt ttgtcctcta attccaggat cctcaaccac cagcagggga      720
243 ccattgccgaa cctgcatgac tactgtctcaa ggaacctcta tgtatccctc ctgttgctgt      780
245 accaaacctt cggacggaaa ttgcacctgt attcccatcc catcatcctg ggctttcgga      840
247 aaattcctat gggagtgggc ctcagcccggt ttctcctggc tcagtttact agtgccattt      900

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/890,752

DATE: 08/14/2001

TIME: 11:17:14

Input Set : A:\PTO.txt

Output Set: N:\CRF3\08142001\I890752.raw

```

249 gttcagtggg tcgtaggggt ttccccact gtttggttt cagttatatg gatgatgtgg      960
251 tattgggggc caagtctgta cagcatcttg agtccctttt taccgctgtt accaattttc      1020
253 ttttgtcttt ggtatacat ttaaacc                                1047
258 <210> SEQ ID NO: 5
259 <211> LENGTH: 35
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Description of the artificial sequence:
265     Primer
269 <400> SEQUENCE: 5
274 ccatattctt gggaacaaga tatccagcac ggggc      35
277 <210> SEQ ID NO: 6
278 <211> LENGTH: 33
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of the artificial sequence:
284     Primer
287 <400> SEQUENCE: 6
289 ggattgctgg tggaagatat ctgccccgtg ctg      33
293 <210> SEQ ID NO: 7
294 <211> LENGTH: 33
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Description of the artificial sequence:
300     Primer
303 <400> SEQUENCE: 7
305 cagcacgggg cagatatctt ccaccagcaa tcc      33
309 <210> SEQ ID NO: 8
310 <211> LENGTH: 38
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of the artificial sequence:
316     Primer
319 <400> SEQUENCE: 8
321 gccccgtgct ggatatcatc ttgttcccaa gaatatgg      38
324 <210> SEQ ID NO: 9
325 <211> LENGTH: 36
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Description of the artificial sequence:
331     Primer
334 <400> SEQUENCE: 9
337 aaaagatctg gccgtggcga aggagctgga gcattc      36
341 <210> SEQ ID NO: 10

```

RAW SEQUENCE LISTING                      DATE: 08/14/2001  
 PATENT APPLICATION: US/09/890,752              TIME: 11:17:14

Input Set : A:\PTO.txt  
 Output Set: N:\CRF3\08142001\I890752.raw

```

342 <211> LENGTH: 30
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: Description of the artificial sequence:
348     Primer
351 <400> SEQUENCE: 10
353 aaaagatctg gtttaaagt atacccaaag          30
356 <210> SEQ ID NO: 11
357 <211> LENGTH: 33
358 <212> TYPE: DNA
359 <213> ORGANISM: Artificial sequence
361 <220> FEATURE:
362 <223> OTHER INFORMATION: Description of the artificial sequence:
363     Primer
366 <400> SEQUENCE: 11
368 cccgatatca tgcattctt tggatcatgta cta          33
371 <210> SEQ ID NO: 12
372 <211> LENGTH: 30
373 <212> TYPE: DNA
374 <213> ORGANISM: Artificial sequence
376 <220> FEATURE:
377 <223> OTHER INFORMATION: Description of the artificial sequence:
378     Primer
381 <400> SEQUENCE: 12
383 ggggatatcg gtcgatgtcc atgccccaaa          30
386 <210> SEQ ID NO: 13
387 <211> LENGTH: 36
388 <212> TYPE: DNA
389 <213> ORGANISM: Artificial sequence
391 <220> FEATURE:
392 <223> OTHER INFORMATION: Description of the artificial sequence:
393     Primer
396 <400> SEQUENCE: 13
399 gggggatccc gatgtacggg ccagatatac gcgttg          36
402 <210> SEQ ID NO: 14
403 <211> LENGTH: 27
404 <212> TYPE: DNA
405 <213> ORGANISM: Artificial sequence
408 <220> FEATURE:
409 <223> OTHER INFORMATION: Description of the artificial sequence:
410     Primer
413 <400> SEQUENCE: 14
415 gggggatccg cggccgcttt acttgta          27
418 <210> SEQ ID NO: 15
419 <211> LENGTH: 57
420 <212> TYPE: DNA
421 <213> ORGANISM: Artificial sequence
423 <220> FEATURE:

```

<210> 17  
<211> 36  
<212> DNA

<213> Artificial sequence Errored

<220>

<223> Description of the artificial sequence:  
Primer

Unknown nucleotides  
must be described in  
fields 221, 222 and 223

<400> 17

nnngaattct ggatcttcca aattaacacc caccca

These types of errors exist  
throughout the sequence listing

The types of errors shown exist throughout the Sequence Listing. Please check  
subsequent sequences for similar errors.

## VERIFICATION SUMMARY

DATE: 08/14/2001

PATENT APPLICATION: US/09/890,752

TIME: 11:17:15

Input Set : A:\PTO.txt

Output Set: N:\CRF3\08142001\I890752.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:430 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15  
L:430 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15  
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:446 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16  
L:446 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16  
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:461 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17  
L:461 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:477 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18  
L:477 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18  
L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:492 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19  
L:492 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19  
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19